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Sequence Listing was accepted.

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217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=4; day=10; hr=11; min=39; sec=17; ms=889; ]

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Application No: 09763824

Version No: 6.0

**Input Set:****Output Set:****Started:** 2009-03-20 16:01:08.590**Finished:** 2009-03-20 16:01:10.390**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 800 ms**Total Warnings:** 36**Total Errors:** 0**No. of SeqIDs Defined:** 42**Actual SeqID Count:** 42

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
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W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
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W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
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**Input Set:**

**Output Set:**

**Started:** 2009-03-20 16:01:08.590  
**Finished:** 2009-03-20 16:01:10.390  
**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 800 ms  
**Total Warnings:** 36  
**Total Errors:** 0  
**No. of SeqIDs Defined:** 42  
**Actual SeqID Count:** 42

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

<110> SQUIRRELL, DAVID J.  
MURPHY, MELANIE J.  
PRICE, RACHEL L.  
LOWE, CHRISTOPHER R.  
WHITE, PETER J.  
TISI, LAURENCE C.  
MURRAY, JAMES A. H .

<120> NOVEL ENZYME

<130> 1498-119

<140> 09763824

<141> 2001-02-27

<150> PCT/GB99/03538

<151> 1999-10-26

<150> GB 9823468.5

<151> 1998-10-28

<160> 42

<170> PatentIn Ver. 2.1

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 1

cgccggtgag ctccccgccg ccg

23

<210> 2

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

<400> 2

cggcggcggg gagctcaccg gcg

23

<210> 3

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 3  
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<210> 4  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Primer

<400> 4  
cctttgtatt taattaaaga cttaaggcgg tcaactatga agaagtgttc g 51

<210> 5  
<211> 32  
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<400> 5  
gaaaggcccg gcaccagcct atcctctaga gg 32

<210> 6  
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<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 6  
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<210> 7  
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<220>  
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<210> 8  
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<220>  
<223> Description of Artificial Sequence: Primer

<400> 8	
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ccgcatagag ctctctgcgt cagattc	27

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gtatagattt gaaaaagagc tg	22
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ggctacatac tggagacata gc	22
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 <400> 21  
 gtcggttcacg ggcgcaactg c 21  
  
 <210> 22  
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<211> 27  
 <212> DNA  
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 <212> DNA  
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 <400> 26  
 ctgattacac ccaaggggga tg 22  
  
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 <400> 27  
 catccccctt ggggtgtaatc ag 22  
  
 <210> 28  
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 <220>  
 <221> modified\_base  
 <222> (15)..(17)  
 <223> a, g, c or t  
  
 <400> 28

cccttcgcga tagannngcc tgcgtcagt 29

<210> 29

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

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<222> (13)..(15)

<223> a, g, c or t

<400> 29

actgacgcag gcnnntctat gcggaaggg 29

<210> 30

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 30

gcaatcaaat cgctccggat actgc 25

<210> 31

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 31

gcagtatccg gagcgatttg attgc 25

<210> 32

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 32

ccattccatc aaggtttttg 20

<210> 33

<211> 20

<212> DNA

<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Primer

<400> 33  
 ccaaaacctt gatggaatgg 20

<210> 34  
 <211> 25  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 34  
 aaacagggac ccatatggaa gacgc 25

<210> 35  
 <211> 36  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 35  
 aattaactcg aggaatttcg tcacgctga atacag 36

<210> 36  
 <211> 30  
 <212> DNA  
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<220>  
 <223> Description of Artificial Sequence: Primer

<400> 36  
 ccctattttc attcctggcc aaaagcactg 30

<210> 37  
 <211> 550  
 <212> PRT  
 <213> Photinus pyralis

<400> 37  
 Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
 1 5 10 15  
 Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
 20 25 30  
 Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45  
 Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
 50 55 60

Glu	Ala	Met	Lys	Arg	Tyr	Gly	Leu	Asn	Thr	Asn	His	Arg	Ile	Val	Val	65	70	75	80
Cys	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Met	Pro	Val	Leu	Gly	Ala	Leu	85	90	95	
Phe	Ile	Gly	Val	Ala	Val	Ala	Pro	Ala	Asn	Asp	Ile	Tyr	Asn	Glu	Arg	100	105	110	
Glu	Leu	Leu	Asn	Ser	Met	Asn	Ile	Ser	Gln	Pro	Thr	Val	Val	Phe	Val	115	120	125	
Ser	Lys	Lys	Gly	Leu	Gln	Lys	Ile	Leu	Asn	Val	Gln	Lys	Lys	Leu	Pro	130	135	140	
Ile	Ile	Gln	Lys	Ile	Ile	Ile	Met	Asp	Ser	Lys	Thr	Asp	Tyr	Gln	Gly	145	150	155	160
Phe	Gln	Ser	Met	Tyr	Thr	Phe	Val	Thr	Ser	His	Leu	Pro	Pro	Gly	Phe	165	170	175	
Asn	Glu	Tyr	Asp	Phe	Val	Pro	Glu	Ser	Phe	Asp	Arg	Asp	Lys	Thr	Ile	180	185	190	
Ala	Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	Gly	Val	195	200	205	
Ala	Leu	Pro	His	Arg	Thr	Ala	Cys	Val	Arg	Phe	Ser	His	Ala	Arg	Asp	210	215	220	
Pro	Ile	Phe	Gly	Asn	Gln	Ile	Ile	Pro	Asp	Thr	Ala	Ile	Leu	Ser	Val	225	230	235	240
Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	Gly	Tyr	Leu	245	250	255	
Ile	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	Tyr	Arg	Phe	Glu	Glu	Glu	Leu	260	265	270	
Phe	Leu	Arg	Ser	Leu	Gln	Asp	Tyr	Lys	Ile	Gln	Ser	Ala	Leu	Leu	Val	275	280	285	
Pro	Thr	Leu	Phe	Ser	Phe	Phe	Ala	Lys	Ser	Thr	Leu	Ile	Asp	Lys	Tyr	290	295	300	
Asp	Leu	Ser	Asn	Leu	His	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	305	310	315	320
Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	Lys	Arg	Phe	His	Leu	Pro	Gly	Ile	325	330	335	
Arg	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Ile	Leu	Ile	Thr	340	345	350	
Pro	Glu	Gly	Asp	Asp	Lys	Pro	Gly	Ala	Val	Gly	Lys	Val	Val	Pro	Phe	355	360	365	

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly  
385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly  
405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe  
420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln  
435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile  
450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu  
465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys  
485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu  
500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly  
515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys  
530 535 540

Gly Gly Lys Ser Lys Leu  
545 550

<210> 38

<211> 550

<212> PRT

<213> Photinus pyralis

<220>

<221> VARIANT

<222> (214)

<223> xaa=an amino acid other than Thr

<400> 38

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala

50		55		60	
Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val					
65		70		75	80
Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu					
	85		90		95
Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg					
	100		105		110
Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val					
	115		120		125
Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro					
	130		135		140
Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly					
145		150		155	160
Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe					
	165		170		175
Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile					
	180		185		190
Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val					
	195		200		205
Ala Leu Pro His Arg Xaa Ala Cys Val Arg Phe Ser His Ala Arg Asp					
	210		215		220
Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val					
225		230		235	240
Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu					
	245		250		255
Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu					
	260		265		270
Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val					
	275		280		285
Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr					
	290		295		300
Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser					
305		310		315	320
Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile					
	325		330		335
Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr					
	340		345		350
Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe					

355

360

365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly  
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly  
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe  
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln  
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile  
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu  
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys  
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu  
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly  
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys  
 530 535 540

Gly Gly Lys Ser Lys Leu  
 545 550

<210> 39

<211> 550

<212> PRT

<213> Photinus pyralis

<220>

<221> VARIANT

<222> (214)

<223> Xaa=Cys, Ala or Asn

<400> 39

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
 1 5 10 15

Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45

Val Asn Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu  
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg  
100 105 110

Glu Leu Leu Asn Ser Met Asn Ile Ser Gln Pro Thr Val Val Phe Val  
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro  
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  
145